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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 23.84 Seconds
(without alignments)
105.641 Million cell updates/sec

Title: US-08-841-657a-2

Perfect score: 176

Sequence: 1 RRRGRPRRTTPSPRRRRKSPRRRRSQRSQCSOC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID88/cgcdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	100.0	34	AAW33686	HBC nucleic acid-b
2	176	100.0	161	AAW33689	Recombinant protei
3	176	100.0	183	AAW33687	Hepatitis B virus
4	176	100.0	183	AAW33688	Hepatitis B virus
5	176	100.0	183	AAW33680	Hepatitis B virus
6	176	100.0	183	AAW33681	Hepatitis B virus
7	176	100.0	183	AAW33682	Hepatitis B virus
8	176	100.0	183	AAW33683	Hepatitis B virus
9	176	100.0	183	AAW33684	Hepatitis B virus
10	176	100.0	183	AAW33685	Hepatitis B virus
11	176	100.0	191	AAW33690	Recombinant protei

12	176	100.0	281	18	AAW33691	Nucleic acid-bound
13	176	100.0	456	18	AAW33693	Nucleic acid-bound
14	172	97.7	183	1	AAP00041	Sequence of core a
15	172	97.7	183	5	AAP40311	Hepatitis virus co
16	172	97.7	183	11	AAW05635	Hepatitis B antige
17	172	97.7	183	14	AAW40805	Hepatitis B core p
18	172	97.7	183	15	AAW62869	Hepatitis B virus
19	172	97.7	183	16	AAW68866	Hepatitis B virus
20	172	97.7	183	16	AAW68868	Hepatitis B virus
21	172	97.7	183	16	AAW68869	Hepatitis B virus
22	172	97.7	183	16	AAW68870	Hepatitis B virus
23	172	97.7	183	16	AAW68871	Hepatitis B virus
24	172	97.7	183	19	AAW50251	Human hepatitis B
25	172	97.7	183	20	AAW29759	Human hepatitis B
26	172	97.7	183	20	AAW29674	Human hepatitis B
27	172	97.7	183	21	AAW35769	Hepatitis b virus
28	172	97.7	183	22	AAW98044	Synthetic hepatitis
29	172	97.7	183	22	AAW80959	Viral protein sequ
30	172	97.7	184	1	AAP00004	Sequence of core a
31	172	97.7	184	9	AAP80959	Hepatitis B virus
32	172	97.7	193	19	AAW50241	Hepatitis B virus
33	172	97.7	194	19	AAW50242	Hepatitis B virus
34	172	97.7	196	14	AAW40806	Hepatitis B core /
35	172	97.7	198	14	AAW40807	Hepatitis B core /
36	172	97.7	198	19	AAW50252	Hepatitis B core /
37	172	97.7	208	14	AAW40808	Hepatitis B core /
38	172	97.7	212	19	AAW50250	Hepatitis B virus
39	172	97.7	212	21	AAW44350	Human hepatitis B
40	172	97.7	212	22	AAW66922	HBV genotype B pre
41	172	97.7	212	22	AAW66923	HBV genotype C pre
42	172	97.7	212	22	AAW66924	HBV genotype D pre
43	172	97.7	346	13	AAW7473	S12/core protein.
44	167	94.9	215	21	AAW10597	HBV fusion protein
45	166	94.3	183	16	AAW68865	Hepatitis B virus

ALIGNMENTS

RESULT 1
AAW33686
ID AAW33686 standard; peptide; 34 AA.
AC AAW33686;
XX
DT 30-APR-1998 (first entry)
DE HBC nucleic acid-binding motif sequence.
XX
KW Nucleic acid-binding motif; Hbc; HBV; Hepatitis B virus; diagnosis;
KW HCV core polypeptide; immunoassay; detection; antigen; disease;
KW Hepatitis C virus; infection.
XX
OS Hepatitis B virus.
PN EP805160-A1.
PD 05-NOV-1997.
XX
PF 30-APR-1997; 97EP-0400985.
PR 01-MAY-1996; 96JP-0134444.
XX (FJRE) FUJIREBIO INC.
XX
PI Itoh S, Takemura F, Ueno E;
DR WPI; 1997-529030/49.
XX N-PSDB; AAW06334.
PT Nucleic acid-bound polypeptide - useful as immunoassay reagent
XX Claim 5; Page 16; 38pp; English.
PS

XX This is a nucleic acid-binding motif present in the Hbc protein of
 CC Hepatitis B virus (HBV). This is fused to one terminus of a Hepatitis C
 CC virus (HCV) core polypeptide. This is used in a method for producing a
 CC nucleic acid-bound polypeptide. The method comprises producing a
 CC fusion gene containing the polypeptide and the nucleic acid-binding
 CC motif, binding a nucleic acid to the polypeptide as a soluble fraction,
 CC and purifying the nucleic acid-bound polypeptide from the soluble
 CC fraction. When the polypeptide is a recombinant form of an antigen, the
 CC nucleic acid-bound polypeptide can be used as an immunoassay reagent for
 CC detecting the antigen or an antibody to the antigen, especially in an
 CC agglutination assay using particles coated with the nucleic acid-bound
 CC polypeptide. The methods can be applied to diagnosis of disease and
 CC infection, especially for the detection of HBV and HCV polypeptides.
 CC The nucleic acid-bound polypeptides may be immunoreactive in cases where
 CC the free polypeptide is not.
 XX Sequence 34 AA;

Query Match 100.0%; Score 176; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.8e-14;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSQSQ 34
 DB 1 rrrgsprrtpsprrrrsksprrrrsqsq 34

RESULT 2

ID AAW33689 standard; Protein: 161 AA.
 AC AAW33689;
 DT 30-APR-1998 (first entry)
 DE Recombinant protein 120NA.
 KW Nucleic acid-binding motif; HCV; HBV; Hepatitis C virus; diagnosis;
 KW core polypeptide; immunoassay; detection; antigen; disease; infection;
 KW Hepatitis B virus; recombinant.
 OS Synthetic.
 OS Chimeric - Hepatitis C virus.
 OS Chimeric - Hepatitis B virus.
 PN EP805160-A1.
 PD 05-NOV-1997.
 PF 30-APR-1997; 97EP-0400985.
 PR 01-MAY-1996; 96JP-0134444.
 PA (FJRE) FUJIREBIO INC.
 PI Itoh S, Takemura F, Ueno E;
 DR WPI; 1997-529030/49.
 DR N-PSDB; AAV06337.
 XX Nucleic acid-bound polypeptide - useful as immunoassay reagent
 XX Example 1; Pages 20-21; 38pp; English.

XX This is a recombinant protein 120NA. This recombinant protein contains
 CC the Hepatitis C virus (HCV) core polypeptide 120 fused to a nucleic
 CC acid-binding motif present in the Hbc protein of Hepatitis B virus
 CC (HBV). This recombinant protein can be bound to a nucleic acid in the
 CC host for producing a nucleic acid-bound polypeptide by a new method.
 CC The method comprises producing a fusion gene containing the polypeptide
 CC and the nucleic acid-binding motif, binding a nucleic acid to the

CC polypeptide as a soluble fraction, and purifying the nucleic acid-bound
 CC polypeptide from the soluble fraction. When the polypeptide is a
 CC recombinant form of an antigen, the nucleic acid-bound polypeptide can be
 CC used as an immunoassay reagent for detecting the antigen or an antibody
 CC to the antigen, especially in an agglutination assay using particles
 CC coated with the nucleic acid-bound polypeptide. The methods can be
 CC applied to diagnosis of disease and infection, especially for the
 CC detection of HBV and HCV polypeptides. The nucleic acid-bound
 CC polypeptides may be immunoreactive in cases where the free polypeptide
 CC is not.
 XX Sequence 161 AA;

Query Match 100.0%; Score 176; DB 18; Length 161;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSQSQ 34
 DB 128 rrrgsprrtpsprrrrsksprrrrsqsq 161

RESULT 3

ID AAR98878 standard; Protein: 183 AA.
 AC AAR98878;
 DT 29-AUG-1996 (first entry)
 DE Hepatitis B virus E antigen (wild-type).
 KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
 KW cross-reactivity.
 OS Hepatitis B virus.
 XX Key Location/Qualifiers
 FT Misc-difference 74..75
 FT /note= "mutation of Ser74 and/or Asn75 results in
 FT a polypeptide having reduced
 FT reactivity with antibodies raised against
 FT HBV C antigen"
 DN JP08027185-A.
 XX 30-JAN-1996.
 XX 11-JUL-1994; 94JP-0180445.
 XX 11-JUL-1994; 94JP-0180445.
 XX (FJRE) FUJI REBIO KK.
 XX WPI; 1996-136327/14.
 XX Novel anti-hepatitis-B-virus-e-antigen mutant for immuno-diagnosis
 PT of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody
 PT without reacting with anti-HBV-c-Ag antibody
 XX Disclosure; Page 5-6; 7pp; Japanese.

XX The present sequence is that of the wild-type e-antigen of
 CC hepatitis B virus. This polypeptide is recognised both by
 CC anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
 CC sensitivity of immunodiagnosis of hepatitis B, at least one of
 CC residues 74 or 75 of the wild-type e-antigen is mutated. The
 CC mutations result in antigens having reduced reactivity with anti-
 CC HBeAg antibodies but which are still recognised by anti-HBeAg
 CC antibodies. See AAR98879-R98885 for preferred mutants.
 XX Sequence 183 AA;

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Query Match      100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQRESQC 34
   |||||
DB 150 rrrgrsprrrtpsprrrrsksprrrrsqresqc 183

RESULT 4
AAR98879
ID AAR98879 standard; protein; 183 AA.
XX
AC AAR98879;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut4 (Lys74, Leu75) mutain.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
KW cross-reactivity; mutain; variant; modified.
XX
OS Hepatitis B virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 74..75
FT /note- "wild-type Ser74 and Asn75 have been
FT replaced by Lys74 and Leu75"
XX
PN JP08027185-A.
XX
PD 30-JAN-1996.
XX
PF 11-JUL-1994; 94JP-0180445.
XX
PR 11-JUL-1994; 94JP-0180445.
XX
PA (FJRE ) FUJI REBIO KK.
XX
PS WPI; 1996-136327/14.
XX
SQ The wild-type e-antigen of hepatitis B virus is recognised both by
anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
sensitivity of immunodiagnosis of hepatitis B, at least one of
residues 74 or 75 of the wild-type e-antigen is mutated. The
mutations result in antigens having reduced reactivity with anti-
HBcAg antibodies (HBcAb) but which are still recognised by anti-HBeAg
antibodies (HBeAb). The present sequence is that of the mut4 mutain
which does not react at all with anti-HBcAb and reacts well with anti-
HBeAb (though not as well as wild-type HBeAg).
XX
SQ Sequence 183 AA;

Query Match      100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQRESQC 34
   |||||
DB 150 rrrgrsprrrtpsprrrrsksprrrrsqresqc 183

RESULT 5
AAR98879
ID AAR98879 standard; protein; 183 AA.
XX
AC AAR98879;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut4 (Lys74, Leu75) mutain.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
KW cross-reactivity; mutain; variant; modified.
XX
OS Hepatitis B virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 74..75
FT /note- "wild-type Ser74 and Asn75 have been
FT replaced by Lys74 and Leu75"
XX
PN JP08027185-A.
XX
PD 30-JAN-1996.
XX
PF 11-JUL-1994; 94JP-0180445.
XX
PR 11-JUL-1994; 94JP-0180445.
XX
PA (FJRE ) FUJI REBIO KK.
XX
PS WPI; 1996-136327/14.
XX
SQ The wild-type e-antigen of hepatitis B virus is recognised both by
anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
sensitivity of immunodiagnosis of hepatitis B, at least one of
residues 74 or 75 of the wild-type e-antigen is mutated. The
mutations result in antigens having reduced reactivity with anti-
HBcAg antibodies (HBcAb) but which are still recognised by anti-HBeAg
antibodies (HBeAb). The present sequence is that of the mut4 mutain
which does not react at all with anti-HBcAb and reacts well with anti-
HBeAb (though not as well as wild-type HBeAg).
XX
SQ Sequence 183 AA;

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AAR98880
ID AAR98880 standard; protein; 183 AA.
XX
AC AAR98880;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut27 (Asn74, Pro75) mutain.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
KW cross-reactivity; mutain; variant; modified.
XX
OS Hepatitis B virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 74..75
FT /note- "wild-type Ser74 and Asn75 have been
FT replaced by Asn74 and Pro75"
XX
PN JP08027185-A.
XX
PD 30-JAN-1996.
XX
PF 11-JUL-1994; 94JP-0180445.
XX
PR 11-JUL-1994; 94JP-0180445.
XX
PA (FJRE ) FUJI REBIO KK.
XX
PS WPI; 1996-136327/14.
XX
SQ Novel anti-hepatitis-B-virus-e-antigen mutant for immuno-diagnosis
of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody
without reacting with anti-HBV-c-Ag antibody
XX
PS Disclosure; Page -: 7pp; Japanese.
XX
CC The wild-type e-antigen of hepatitis B virus is recognised both by
anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
sensitivity of immunodiagnosis of hepatitis B, at least one of
residues 74 or 75 of the wild-type e-antigen is mutated. The
mutations result in antigens having reduced reactivity with anti-
HBcAg antibodies (HBcAb) but which are still recognised by anti-HBeAg
antibodies (HBeAb). The present sequence is that of the mut27 mutain
which does not react at all with anti-HBcAb and reacts well with anti-
HBeAb (though not as well as wild-type HBeAg).
XX
SQ Sequence 183 AA;

Query Match      100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQRESQC 34
   |||||
DB 150 rrrgrsprrrtpsprrrrsksprrrrsqresqc 183

RESULT 6
AAR98881
ID AAR98881 standard; protein; 183 AA.
XX
AC AAR98881;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut28 (Ser74, Leu75) mutain.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
KW cross-reactivity; mutain; variant; modified.
XX

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OS Hepatitis B virus.
 XX Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 74..75
 FT /note= "wild-type Ser74 is not changed and Asn75 is
 FT replaced by Leu75"
 XX
 XX JP08027185-A.
 XX
 XX 30-JAN-1996.
 XX
 XX 11-JUL-1994; 94JP-0180445.
 XX
 XX 11-JUL-1994; 94JP-0180445.
 XX
 XX (FJRE) FUJI REBIO KK.
 XX
 XX WPI; 1996-136327/14.
 XX
 XX Novel anti-hepatitis-B-virus-e-antigen mutant for immuno:diagnosis
 PT of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody
 PT without reacting with anti-HBV-c-Ag antibody
 XX
 PS Disclosure; Page : 7pp; Japanese.
 XX
 XX The wild-type e-antigen of hepatitis B virus is recognised both by
 CC anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
 CC sensitivity of immunodiagnosis of hepatitis B, at least one of
 CC residues 74 or 75 of the wild-type e-antigen is mutated. The
 CC mutations result in antigens having reduced reactivity with anti-
 CC HBcAg antibodies (HBcAb) but which are still recognised by anti-
 CC HBsAg antibodies (HBsAb). The present sequence is that of the mut28 mutein
 CC which does not react at all with anti-HBcAb and reacts well with anti-
 CC HBeAb (though not as well as wild-type HBeAg).
 XX
 SQ Sequence 183 AA;
 Query Match 100.0%; Score 176; DB 17; Length 183;
 Best Local Similarity 100.0%; Pred. No. 2.1e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQRESQC 34
 |||||
 DB 150 rrrgrsprrrtpsprrrrsksprrrrsqresqc 183
 RESULT 7
 AAR98882
 ID AAR98882 standard; protein; 183 AA.
 XX
 AC AAR98882;
 XX
 DT 29-AUG-1996 (first entry)
 XX
 DE Hepatitis B virus E antigen mut102 (Cys74, Tyr75) mutein.
 XX
 KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
 KW cross-reactivity; mutein; variant; modified.
 XX
 OS Hepatitis B virus.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 74..75
 FT /note= "wild-type Ser74 and Asn75 have been
 FT replaced by Cys74 and Tyr75"
 XX
 XX JP08027185-A.
 XX
 XX 30-JAN-1996.
 XX

PF 11-JUL-1994; 94JP-0180445.
 XX
 PR 11-JUL-1994; 94JP-0180445.
 XX
 PA (FJRE) FUJI REBIO KK.
 XX
 DR WPI; 1996-136327/14.
 XX
 XX Novel anti-hepatitis-B-virus-e-antigen mutant for immuno:diagnosis
 PT of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody
 PT without reacting with anti-HBV-c-Ag antibody
 XX
 PS Disclosure; Page : 7pp; Japanese.
 XX
 XX The wild-type e-antigen of hepatitis B virus is recognised both by
 CC anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
 CC sensitivity of immunodiagnosis of hepatitis B, at least one of
 CC residues 74 or 75 of the wild-type e-antigen is mutated. The
 CC mutations result in antigens having reduced reactivity with anti-
 CC HBcAg antibodies (HBcAb) but which are still recognised by anti-
 CC HBsAg antibodies (HBsAb). The present sequence is that of the mut102 mutein
 CC which does not react at all with anti-HBcAb and reacts well with anti-
 CC HBeAb (though not as well as wild-type HBeAg).
 XX
 SQ Sequence 183 AA;
 Query Match 100.0%; Score 176; DB 17; Length 183;
 Best Local Similarity 100.0%; Pred. No. 2.1e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQRESQC 34
 |||||
 DB 150 rrrgrsprrrtpsprrrrsksprrrrsqresqc 183
 RESULT 8
 AAR98883
 ID AAR98883 standard; protein; 183 AA.
 XX
 AC AAR98883;
 XX
 DT 29-AUG-1996 (first entry)
 XX
 DE Hepatitis B virus E antigen mut30 (Ser74, Glu75) mutein.
 XX
 KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
 KW cross-reactivity; mutein; variant; modified.
 XX
 OS Hepatitis B virus.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 74..75
 FT /note= "wild-type Ser74 is not changed and Asn75 is
 FT replaced by Glu75"
 XX
 XX JP08027185-A.
 XX
 XX 30-JAN-1996.
 XX
 XX 11-JUL-1994; 94JP-0180445.
 XX
 XX 11-JUL-1994; 94JP-0180445.
 XX
 XX (FJRE) FUJI REBIO KK.
 XX
 DR WPI; 1996-136327/14.
 XX
 XX Novel anti-hepatitis-B-virus-e-antigen mutant for immuno:diagnosis
 PT of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody
 PT without reacting with anti-HBV-c-Ag antibody
 XX

PS Disclosure; Page -: 7pp; Japanese.

CC The wild-type e-antigen of hepatitis B virus is recognised both by anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the sensitivity of immunodiagnosis of hepatitis B, at least one of residues 74 or 75 of the wild-type e-antigen is mutated. The mutations result in antigens having reduced reactivity with anti-HBcAg antibodies (HBcAb) but which are still recognised by anti-HBeAg antibodies (HBeAb). The present sequence is that of the mut30 mutein which has reduced reactivity with anti-HBcAb but retains reactivity with anti-HBeAb equivalent to that of the wild-type antigen.

SQ Sequence 183 AA;

Query Match 100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRSSQC 34
|||||
Db 150 rrrgrsprtptpsrrrrsksprrrrsqsrsc 183

RESULT 9

AAR98884

ID AAR98884 standard; protein; 183 AA.

AC AAR98884;

XX

DT 29-AUG-1996 (first entry)

DE Hepatitis B virus E antigen mut32 (Asp74, His75) mutein.

XX

KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
cross-reactivity; mutein; variant; modified.

XX

OS Hepatitis B virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 74..75

FT /note= "wild-type Ser74 and Asp75 have been replaced by Asp74 and His75"

FT

XX

PN JP08027185-A.

XX

PD 30-JAN-1996.

XX

PF 11-JUL-1994; 94JP-0180445.

XX

PR 11-JUL-1994; 94JP-0180445.

XX

PA (FJRE) FUJI REBIO KK.

XX

DR WPI; 1996-136327/14.

XX

Novel anti-hepatitis-B-virus-e-antigen mutant for immuno-diagnosis of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody without reacting with anti-HBV-c-Ag antibody

PS Disclosure; Page -: 7pp; Japanese.

CC The wild-type e-antigen of hepatitis B virus is recognised both by anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the sensitivity of immunodiagnosis of hepatitis B, at least one of residues 74 or 75 of the wild-type e-antigen is mutated. The mutations result in antigens having reduced reactivity with anti-HBcAg antibodies (HBcAb) but which are still recognised by anti-HBeAg antibodies (HBeAb). The present sequence is that of the mut32 mutein which has reduced reactivity with anti-HBcAb but retains reactivity with anti-HBeAb equivalent to that of the wild-type antigen.

SQ Sequence 183 AA;

Query Match 100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRSSQC 34
|||||
Db 150 rrrgrsprtptpsrrrrsksprrrrsqsrsc 183

RESULT 10

AAR98885

ID AAR98885 standard; protein; 183 AA.

XX

AC AAR98885;

XX

DT 29-AUG-1996 (first entry)

DE Hepatitis B virus E antigen mut34 (Glu74, Ala75) mutein.

XX

KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
cross-reactivity; mutein; variant; modified.

XX

OS Hepatitis B virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 74..75

FT /note= "wild-type Ser74 and Asp75 have been replaced by Glu74 and Ala75"

FT

XX

PN JP08027185-A.

XX

PD 30-JAN-1996.

XX

PF 11-JUL-1994; 94JP-0180445.

XX

PR 11-JUL-1994; 94JP-0180445.

XX

PA (FJRE) FUJI REBIO KK.

XX

DR WPI; 1996-136327/14.

XX

Novel anti-hepatitis-B-virus-e-antigen mutant for immuno-diagnosis of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody without reacting with anti-HBV-c-Ag antibody

PS Disclosure; Page -: 7pp; Japanese.

CC The wild-type e-antigen of hepatitis B virus is recognised both by anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the sensitivity of immunodiagnosis of hepatitis B, at least one of residues 74 or 75 of the wild-type e-antigen is mutated. The mutations result in antigens having reduced reactivity with anti-HBcAg antibodies (HBcAb) but which are still recognised by anti-HBeAg antibodies (HBeAb). The present sequence is that of the mut34 mutein which has reduced reactivity with anti-HBcAb but retains reactivity with anti-HBeAb equivalent to that of the wild-type antigen.

OS Synthetic.
 OS Chimeric - Treponema pallidum.
 OS Chimeric - Hepatitis B virus.
 XX
 PN EP805160-A1.
 XX
 XX 05-NOV-1997.
 PD
 XX 30-APR-1997; 97EP-0400985.
 PF
 XX 01-MAY-1996; 96JP-0134444.
 PR
 XX (FJRE) FUJIREBIO INC.
 XX
 XX Itoh S, Takemura F, Ueno E;
 PI
 XX WPI: 1997-529030/49.
 DR
 XX N-PSDB; AAN06341.
 DR

PT Nucleic acid-bound polypeptide - useful as immunoassay reagent
 XX
 XX Example 12; Pages 30-31; 38pp; English.

XX This is a nucleic acid-bound polypeptide TP47C2NA. This contains the
 CC Treponema pallidum 47 kDa antigen and a nucleic acid-binding motif
 CC present in the HBC protein of Hepatitis B virus (HBV). This nucleic
 CC acid-bound polypeptide can be produced by a new method. The method
 CC comprises producing a fusion gene containing the polypeptide and the
 CC nucleic acid-binding motif, binding the nucleic acid to the polypeptide as
 CC the soluble fraction, and purifying the nucleic acid-bound polypeptide from
 CC the soluble fraction. When the polypeptide is a recombinant form of an
 CC antigen, the nucleic acid-bound polypeptide can be used as an immunoassay
 CC reagent for detecting the antigen or an antibody to the antigen.
 CC especially in an agglutination assay using particles coated with the
 CC nucleic acid-bound polypeptide. The methods can be applied to diagnosis
 CC of disease and infection, especially for the detection of HBV and HCV
 CC polypeptides. The nucleic acid-bound polypeptides may be immunoreactive
 CC in cases where the free polypeptide is not.

XX Sequence 456 AA;

Query Match 100.0%; Score 176; DB 18; Length 456;
 Best Local Similarity 100.0%; Pred. No. 4.9e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34
 |||||
 Db 423 rrrgrsprtpsprrrsksprrrrsqsresqc 456

RESULT 14

AAFP00041
 ID AAFP00041 standard; Protein; 183 AA.

XX
 AC AAFP00041;

XX 14-OCT-1992 (first entry)

XX Sequence of core antigen.

XX Hepatitis B virus; antigen; antibody; diagnosis; vaccine.

XX Hepatitis B virus.

XX EPI3828-A.

XX 06-AUG-1980.

XX 21-DEC-1979; 79EP-0303017.

XX 01-NOV-1979; 79GB-0037910.

PR 22-DEC-1978; 78GB-0049907.

PR 27-DEC-1978; 78GB-0050039.

XX (BIOJ) BIOGEN NV.

XX Murray K, Schaller HE;

XX WPI: 1980-57268C/33.

XX N-PSDB; AAN00003.

XX Recombinant DNA coding for polypeptide - have specificity of
 PT hepatitis B viral antigens in detection or antibody stimulation

XX Example; Figs 3-4; 43pp; English.

XX Human serum from a single HBsAg positive, HBeAg positive donor
 CC (serotype adym) was used to prep. a DNA-contg. pellet which was
 CC labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
 CC The labelled DNA was then extracted with phenol from the resulting
 CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
 CC It was then cloned in plasmid pBR322 which was used to transform E.
 CC coli. Micro-organisms prepd. by the processes are deposited at the
 CC NCIB as pBR322-HBV-G-L e.g. E. coli HB101/pBR322-est I dg;
 CC HBV-Kpn I dg; Tetr Amps HBV+.

XX Sequence 183 AA;

Query Match 97.7%; Score 172; DB 1; Length 183;
 Best Local Similarity 97.1%; Pred. No. 6.2e-13;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34
 |||||
 Db 150 rrrgrsprtpsprrrsksprrrrsqsresqc 183

RESULT 15

AAFP40311

ID AAFP40311 standard; Protein; 183 AA.

XX
 AC AAFP40311;

XX 18-AUG-1992 (first entry)

XX Hepatitis virus core antigen.

XX HBcAg; vaccine; diagnosis; HBV infection.

XX Hepatitis b virus.

XX JP59074985-A.

XX 27-APR-1984.

XX 19-OCT-1982; 82JP-0183432.

XX 19-OCT-1982; 82JP-0183432.

XX (TAKE) TAKEDA CHEMICAL IND KK.

XX WPI: 1984-143231/23.

XX DNA used in prevention of infections by hepatitis virus B -
 PT comprises structural gene of hepatitis virus adr B surface antigen
 PT coding gene and at least 1 virus core antigen structural gene.

XX Disclosure; Fig 3; 13pp; Japanese.

XX The sequence is that of hepatitis virus core antigen (HBcAg). It
 CC can be used as a vaccine for the prevention of infections by
 CC hepatitis B virus (HBV) and also in the diagnosis of early stages
 CC of HBV infection. See also AAFP40310.

SQ Sequence 183 AA:

Query Match 97.78; Score 172; DB 5; Length 183;
 Best Local Similarity 97.18; Freq. No. 6.2e-13;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGRSPRRTPSPRRRSQRRSQ 34
 Db 150 rrrgrsprrtpsprrrsqrrrsqc 183

Search completed: April 18, 2002, 09:27:24
 Job time: 32 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 12.43 seconds
(without alignments)
61.554 Million cell updates/sec

Title: US-08-841-657A-2
Perfect score: 176
Sequence: 1 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents RA.*

- 1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/6C-COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/6D-COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	97.7	39	3	US-08-968-747-5
2	172	97.7	183	3	US-08-968-747-20
3	172	97.7	183	4	US-09-248-588-2
4	172	97.7	183	4	US-09-248-588-4
5	172	97.7	193	3	US-08-968-747-2
6	172	97.7	193	3	US-08-968-747-18
7	172	97.7	193	3	US-08-968-747-21
8	172	97.7	212	3	US-08-968-747-3
9	172	97.7	346	1	US-08-105-483-217
10	172	97.7	346	1	US-08-709-209-217
11	172	97.7	346	1	US-08-458-101-217
12	165	93.8	183	5	PCT-US96-10602-12
13	165	93.8	185	1	US-07-739-642-2
14	165	93.8	185	1	US-07-739-642-4
15	165	93.8	185	1	US-07-739-642-8
16	165	93.8	185	1	US-07-739-642-10
17	165	93.8	185	1	US-07-739-643-2
18	165	93.8	185	1	US-07-739-643-4
19	165	93.8	185	1	US-07-739-643-8
20	165	93.8	185	1	US-07-739-643-10
21	165	93.8	185	1	US-07-739-142-2
22	165	93.8	185	1	US-07-739-142-4
23	165	93.8	185	1	US-07-739-142-8
24	165	93.8	185	1	US-07-739-142-10
25	165	93.8	185	4	US-09-248-588-6
26	163	92.6	211	6	5196194-13
27	149	84.7	397	5	PCT-US96-10602-6

28	141.5	80.4	217	4	US-09-248-588-9	Sequence 9, Appl
29	139.5	79.3	188	4	US-09-248-588-7	Sequence 7, Appl
30	136	77.3	289	5	PCT-US96-10602-8	Sequence 8, Appl
31	91	51.7	351	5	PCT-US96-10602-4	Sequence 4, Appl
32	87	49.4	346	5	PCT-US96-10602-2	Sequence 2, Appl
33	68	38.6	882	4	US-09-413-814-78	Sequence 78, Appl
34	67	38.1	140	2	US-08-557-309B-33	Sequence 33, Appl
35	67	38.1	140	3	US-08-834-306-33	Sequence 33, Appl
36	66	37.5	140	4	US-08-593-674A-33	Sequence 33, Appl
37	66	37.5	657	4	US-07-751-891B-14	Sequence 14, Appl
38	66	37.5	432	2	US-08-933-750C-47	Sequence 47, Appl
39	65.5	37.2	432	4	US-09-234-613-47	Sequence 47, Appl
40	65.5	37.2	432	4	US-09-248-588-13	Sequence 13, Appl
41	65	36.9	305	4	US-09-248-588-13	Sequence 13, Appl
42	64	36.4	301	2	US-08-656-906-35	Sequence 25, Appl
43	64	36.4	301	4	US-09-217-847-35	Sequence 25, Appl
44	64	36.4	614	5	PCT-US95-03236-21	Sequence 21, Appl
45	63	35.8	420	5	PCT-US96-10602-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-968-747-5
; Sequence 5, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-747-5

Query Match 97.7%; Score 172; DB 3; Length 39;
Best Local Similarity 97.1%; Pred No. 7.9e-15;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 34
Db 6 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 39

```

RESULT 2
US-08-968-747-20
; Sequence 20, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/968,747
; APPLICATION NUMBER: 60/074537
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-747-20

Query Match          97.7%; Score 172; DB 3; Length 183;
Best Local Similarity 97.1%; Pred. No. 3.7e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 34
   |||||
Db 150 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 3
US-08-968-747-20
; Sequence 2, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-08-968-747-20

Query Match          97.7%; Score 172; DB 3; Length 183;
Best Local Similarity 97.1%; Pred. No. 3.7e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 34
   |||||
Db 150 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 4
US-09-248-588-4
; Sequence 4, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-4

Query Match          97.7%; Score 172; DB 4; Length 183;
Best Local Similarity 97.1%; Pred. No. 3.7e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 34
   |||||
Db 150 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 5
US-08-968-747-2
; Sequence 2, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-747-20

Query Match          97.7%; Score 172; DB 3; Length 183;
Best Local Similarity 97.1%; Pred. No. 3.7e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 34
   |||||
Db 150 RRRGSPRRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 6
US-09-248-588-2
; Sequence 2, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-2

Query Match 97.7%; Score 172; DB 3; Length 193;
Best Local Similarity 97.1%; Pred. No. 3.9e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
DB 160 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 193

RESULT 6

US-08-968-747-18
Sequence 18, Application US/08968747
Patent No. 6060595

GENERAL INFORMATION:
APPLICANT: Scaglioni et al.
TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,747
FILING DATE: 03-SEP-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/705001

TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-18

Query Match 97.7%; Score 172; DB 3; Length 194;
Best Local Similarity 97.1%; Pred. No. 3.9e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
DB 161 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 194

RESULT 7

US-08-968-747-21
Sequence 21, Application US/08968747
Patent No. 6060595

GENERAL INFORMATION:
APPLICANT: Scaglioni et al.
TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,747
FILING DATE: 03-SEP-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/705001
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-968-747-21

Query Match 97.7%; Score 172; DB 3; Length 199;
Best Local Similarity 97.1%; Pred. No. 4e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
DB 166 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 199

RESULT 8

US-08-968-747-3
Sequence 3, Application US/08968747
Patent No. 6060595

GENERAL INFORMATION:
APPLICANT: Scaglioni et al.
TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,747
FILING DATE: 03-SEP-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08472/705001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-3

Query Match 97.7%; Score 172; DB 3; Length 212;
Best Local Similarity 97.1%; Pred. No. 4.3e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRTPSPRRRSQSPRRRSQSQ 34
DB 179 RRGSPRRTPSPRRRSQSPRRRSQSQ 212

RESULT 9
US-08-105-483-217
Sequence 217, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-105-483-217
Query Match 97.7%; Score 172; DB 1; Length 346;
Best Local Similarity 97.1%; Pred. No. 7e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRGSPRRTPSPRRRSQSPRRRSQSQ 34

US-08-105-483-217
Query Match 97.7%; Score 172; DB 1; Length 346;
Best Local Similarity 97.1%; Pred. No. 7e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRTPSPRRRSQSPRRRSQSQ 34

DB 313 RRGSPRRTPSPRRRSQSPRRRSQSQ 346

RESULT 10
US-08-709-209-217
Sequence 217, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-709-209-217
Query Match 97.7%; Score 172; DB 1; Length 346;
Best Local Similarity 97.1%; Pred. No. 7e-14;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRTPSPRRRSQSPRRRSQSQ 34
DB 313 RRGSPRRTPSPRRRSQSPRRRSQSQ 346

RESULT 11
US-08-458-101-217
Sequence 217, Application US/08458101
Patent No. 5766599
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Perkus, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: No. 5766599ton, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.

APPLICANT: Johnson, Gerard P.
 APPLICANT: Pincus, Steven E.
 APPLICANT: Cox, William I.
 APPLICANT: Audonnet, Jean-Christophe Francis
 APPLICANT: Gettig, Russell Robert
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtiss, Morris & Safford
 ADDRESSEE: c/o William S. Frommer
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2740
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 217:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-458-101-217

Query Match 97.7%; Score 172; DB 1; Length 346;
 Best Local Similarity 97.1%; Pred. No. 7e-14; 0; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 17

QY 1 RRGSRPRRTTSPRRRSKSPRRRSQSQ 34
 DB 313 RRGSRPRRTTSPRRRSKSPRRRSQSQ 346

RESULT 12
 PCT-US96-10602-12
 Sequence 12, Application PC/TUS9610602
 GENERAL INFORMATION:
 APPLICANT: The General Hospital Corporation
 TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10602
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/017,814
 FILING DATE: 20-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00786/282001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 183 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-10602-12

Query Match 93.8%; Score 165; DB 5; Length 183;
 Best Local Similarity 94.1%; Pred. No. 2.6e-13;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSKSPRRRSQSQ 34
 DB 150 RRGSRPRRTTSPRRRSKSPRRRSQSQ 183

RESULT 13
 US-07-739-642-2
 Sequence 2, Application US/07739642
 Patent No. 5173427
 GENERAL INFORMATION:
 APPLICANT: Mallonco, Richard L.
 TITLE OF INVENTION: Vectors And Hosts With Increased
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Richard R. Rodrick
 STREET: 1 Becton Drive
 CITY: Franklin Lakes
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07417-1880
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/739,642
 FILING DATE: 19910801
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Stierwalt, Brian K.
 REGISTRATION NUMBER: 33,213
 REFERENCE/DOCKET NUMBER: P-2272
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-848-5317
 TELEFAX: 201-848-9228
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 185 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 US-07-739-642-2

Query Match 93.8%; Score 165; DB 1; Length 185;
 Best Local Similarity 94.1%; Pred. No. 2.6e-13;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
 Db 152 RDGRSPRRRTSPRRRSKSPRRRSQSRESQC 185

RESULT 14

US-07-739-642-4
 ; Sequence 4, Application US/07739642
 ; Patent No. 5173427
 ; GENERAL INFORMATION:
 ; APPLICANT: Mallonee, Richard L.
 ; TITLE OF INVENTION: Vectors And Hosts With Increased
 ; TITLE OF INVENTION: Expression Of HbcAg
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Richard R. Rodrick
 ; STREET: 1 Becton Drive
 ; CITY: Franklin Lakes
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 07417-1880

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/739,642
 FILING DATE: 19910801
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Stierwalt, Brian K.
 REGISTRATION NUMBER: 33,213
 REFERENCE/DOCKET NUMBER: P-2272
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-848-5317
 TELEFAX: 201-848-9228
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 185 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 US-07-739-642-4

Query Match 93.8%; Score 165; DB 1; Length 185;
 Best Local Similarity 94.1%; Pred. No. 2.6e-13;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
 Db 152 RDGRSPRRRTSPRRRSKSPRRRSQSRESQC 185

RESULT 15

US-07-739-642-8
 ; Sequence 8, Application US/07739642
 ; Patent No. 5173427
 ; GENERAL INFORMATION:
 ; APPLICANT: Mallonee, Richard L.
 ; TITLE OF INVENTION: Vectors And Hosts With Increased
 ; TITLE OF INVENTION: Expression Of HbcAg
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Richard R. Rodrick
 ; STREET: 1 Becton Drive
 ; CITY: Franklin Lakes
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 07417-1880
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/739,642
 FILING DATE: 19910801
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Stierwalt, Brian K.
 REGISTRATION NUMBER: 33,213
 REFERENCE/DOCKET NUMBER: P-2272
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-848-5317
 TELEFAX: 201-848-9228
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 185 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 US-07-739-642-8

Query Match 93.8%; Score 165; DB 1; Length 185;
 Best Local Similarity 94.1%; Pred. No. 2.6e-13;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
 Db 152 RDGRSPRRRTSPRRRSKSPRRRSQSRESQC 185

Search completed: April 18, 2002, 09:28:04
 Job time: 72 sec

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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:28:52 ; Search time 10.17 Seconds
(without alignments)
122.577 Million cell updates/sec

Title: US-08-841-657A-2

Perfect score: 176

Sequence: 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRSSOC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	172	97.7	183	1	CORA_HPBV4
2	172	97.7	183	1	CORA_HPBV1
3	172	97.7	183	1	CORA_HPBV0
4	172	97.7	183	1	CORA_HPBV2
5	172	97.7	183	1	CORA_HPBV3
6	170	96.6	195	1	CORA_HPBV4
7	169	96.0	211	1	CORA_HPBV5
8	165	93.8	185	1	CORA_HPBV6
9	165	93.8	185	1	CORA_HPBV7
10	139	90.3	214	1	CORA_HPBV8
11	139	90.3	212	1	CORA_HPBV9
12	138	89.8	185	1	CORA_HPBV0
13	141.5	80.4	217	1	CORA_HPBV1
14	139.5	79.3	188	1	CORA_HPBV2
15	135	76.7	187	1	CORA_HPBV3
16	105	59.7	196	1	SFR2_CAEEL
17	98.5	56.0	484	1	SFR2_HUMAN
18	95.5	54.3	208	1	YSX2_CAEEL
19	82	46.6	77	1	PRT2_SPOF
20	76.5	43.5	951	1	SFR2_HUMAN
21	76	43.2	61	1	PCFE_HUMAN
22	76	43.2	1654	1	SFR2_HUMAN
23	73	42.6	221	1	SFR2_CHICK
24	73	42.6	221	1	SFR2_HUMAN
25	73	42.6	221	1	SFR2_MOUSE
26	74.5	42.3	78	1	PRT1_SPOF
27	74.5	42.3	739	1	DD15_CAEEL
28	73.5	41.8	1523	1	SON_HUMAN
29	73	41.5	60	1	HSPL_MACGI
30	73	41.5	61	1	HSPL_MACRG
31	72.5	41.2	303	1	SFR1_ARATH
32	72	40.9	483	1	VE2_HPV14
33	72	40.9	503	1	VE2_HPV21

34 71.5 40.6 91 1 PHIL_MYTED
35 71 40.3 57 1 HSP1_DIDMA
36 71 40.3 61 1 HSP_CHICK
37 71 40.3 164 1 SFR3_HUMAN
38 71 40.3 356 1 RS41_ARATH
39 70.5 40.1 498 1 VE2_HPV08
40 69 39.2 238 1 SFR7_HUMAN
41 68 38.6 1200 1 DD15_CAEEL
42 68 38.6 303 1 CORA_HPBDC
43 68 38.6 305 1 CORA_HPBDC
44 68 38.6 350 1 RS40_ARATH
45 68 38.6 1042 1 SUWA_DROME

ALIGNMENTS

RESULT 1
CORA_HPBV4
ID CORA_HPBV4 STANDARD; PRT; 183 AA.
AC P03150; P03151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Hepatitis B virus (subtype adr4), Hepatitis B virus (subtype adr), and
OS Hepatitis B virus (subtype adr / strain Indonesia/PIDW420).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409, 106820, 10412;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ADR:
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.:
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adr.",
RL Nucleic Acids Res. 11:1747-1757(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ADR4;
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyahara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.,
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.",
RL Nucleic Acids Res. 11:4601-4610(1983).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ADW;
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakagawa H., Sastrosowigno R.I., Imai M.,
RA Miyakawa Y., Mayumi M.,
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes",
RL J. Gen. Virol. 69:2575-2583(1988).
RN [4]
RP SEQUENCE FROM N.A.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; V00867; ; NOT_ANNOTATED_CDS.
CC EMBL; X01587; CAA25745.1; ;
CC EMBL; D00331; ; NOT_ANNOTATED_CDS.
CC PIR; A93480; NKVL45.
CC PIR; B93460; NKVL44.
CC PIR; C28925; NKVLJ3.
CC InterPro: IPR002006; Hepatitis_core.
CC Pfam: PF00906; Hepatitis_core; 1.


```

KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21095 MW; ED2DALDB07FB596D CRC64;

Query Match
Best Local Similarity 97.7%; Score 172; DB 1; Length 183;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
    |||||
DB 150 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 183

RESULT 2
COR_A_HPBVO STANDARD; PRT; 183 AA.
AC P17391;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE CORE ANTIGEN.
OS Hepatitis B virus (subtype adv / strain Japan/pJDN233).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M., Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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DR EMBL; D00329; -, NOT_ANNOTATED_CDS.
DR PIR; A28925; NKVLJ1.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match
Best Local Similarity 97.7%; Score 172; DB 1; Length 183;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
    |||||
DB 150 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 183

RESULT 3
COR_A_HPBVO STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE CORE ANTIGEN.
OS Hepatitis B virus (subtype adv / strain Okinawa/pODW282).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M., Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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DR EMBL; D00329; -, NOT_ANNOTATED_CDS.
DR PIR; A28925; NKVLJ1.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match
Best Local Similarity 97.7%; Score 172; DB 1; Length 183;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
    |||||
DB 150 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 183

RESULT 4
COR_A_HPBVO STANDARD; PRT; 183 AA.
AC P03146;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw) cloned in E. coli.";
RL Nature 281:646-650(1979).
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DR EMBL; V01460; CAA24706.1; ALT_INIT.
DR EMBL; X02496; -, NOT_ANNOTATED_CDS.

```

DR PIR; A03711; NKVLAH.
 DR PIR; A03712; NKVLAH.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 162 169
 FT REPEAT 170 177
 FT REPEAT 174 181
 FT CONFLICT 33 33
 FT CONFLICT 80 80
 FT CONFLICT 80 80
 SQ SEQUENCE 183 AA; 21116 MW; E0D9D9763F24E958 CRC64;

Query Match 97.7%; Score 172; DB 1; Length 183;
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRPTSPRRRSKSPRRRSQSRESQC 34
 DB 150 RRGSPRRPTSPRRRSKSPRRRSQSRESQC 183

RESULT 5
 ID CORA_HPBVZ STANDARD; PRT: 183 AA.
 AC P03147;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DE CORE ANTIGEN.
 GN C.

OS Hepatitis B virus (subtype adv2).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10419;

RP SEQUENCE FROM N.A.
 RX MEDLINE=8101215; PubMed=399329;
 RA Pask M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,
 RA Leadbetter G., Murray K.;
 RT "Hepatitis B virus genes and their expression in E. coli.";
 RL Nature 282:575-579(1979).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; J02202; AAA45486.1;
 DR EMBL; A08967; CAA00816.1;
 DR PIR; B93217; NKVLA2.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 162 169
 FT REPEAT 170 177
 SQ SEQUENCE 183 AA; 21042 MW; 545ED0E5527F76C CRC64;

Query Match 97.7%; Score 172; DB 1; Length 183;
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRPTSPRRRSKSPRRRSQSRESQC 34
 DB 150 RRGSPRRPTSPRRRSKSPRRRSQSRESQC 183

RESULT 6
 ID CORA_HPBVZ STANDARD; PRT: 195 AA.
 AC P29178;

DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE CORE ANTIGEN.
 GN C.
 OS Hepatitis B virus (subtype adv2 variant sf).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=31515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9016950; PubMed=2307406;
 RA Bhat R.A., Ulrich P., Vyas G.N.;
 RT "Molecular characterization of a new variant of hepatitis B virus in
 RT a persistently infected homosexual man.";
 RL Hepatology 11:271-276(1990).
 DR PIR; A37182; NKVLA3.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 174 181
 FT REPEAT 182 189
 FT REPEAT 182 189
 SQ SEQUENCE 195 AA; 22461 MW; E2B156F879CB7CB7 CRC64;

Query Match 96.6%; Score 170; DB 1; Length 195;
 Best Local Similarity 97.1%; Pred. No. 3.3e-12;
 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSPRRPTSPRRRSKSPRRRSQSRESQC 34
 DB 162 RRGSPRRPTSPRRRSKSPRRRSQSRESQC 195

RESULT 7
 ID CORA_HPBVA STANDARD; PRT: 211 AA.
 AC P24023;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CORE ANTIGEN.
 GN C.

OS Hepatitis B virus (strain alpha).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10411;

RP SEQUENCE FROM N.A.
 RX MEDLINE=90266476; PubMed=2345966;
 RA Tong S., Li J., Vitvitski L., Trepo C.;
 RT "Active hepatitis B virus replication in the presence of anti-HBe is
 RT associated with viral variants containing an inactive pre-C region.";
 RL Virology 176:596-603(1990).
 CC -----

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 CC -----

DR EMBL; M32138; -; NOT_ANNOTATED_CDS.
 DR PIR; A34773; NKVLA1.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 183 190
 FT REPEAT 198 206
 SQ SEQUENCE 211 AA; 24208 MW; B774AC72E65C75AB CRC64;

Query Match 96.0%; Score 169; DB 1; Length 211;
 Best Local Similarity 94.1%; Pred. No. 4.6e-12;

Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
 |||||
 DB 178 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 211

RESULT 8

CORA_HPBVW STANDARD; PRT; 185 AA.
 ID AC P03149;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DE CORE ANTIGEN.
 GN C.

OS Hepatitis B virus (subtype adw).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=106921;
 RN [1]

RP MEDLINE=63168919; PubMed=6300776;
 RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishiohara K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA; subtype adw and adw.";
 RL Nucleic Acids Res 11:1747-1757(1983).

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CC EMBL; V00866; -; NOT_ANNOTATED_CDS.
 DR PIR; C93460; NKVLA6.

DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.

KW Core protein; Repeat.
 FT REPEAT 164 171
 FT REPEAT 172 179

SQ SEQUENCE 185 AA; 21394 MW; B86A90D541BA70F9 CRC64;
 Query Match 93.8%; Score 165; DB 1; Length 185;
 Best Local Similarity 94.1%; Pred. No. 1.1e-11;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
 |||||
 DB 152 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 185

RESULT 9

CORA_HPBV9 STANDARD; PRT; 214 AA.
 ID AC P17099;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE CORE ANTIGEN.
 GN C.

OS Hepatitis B virus (subtype adw / strain 991).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10410;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Koehel H.G., Schueler A., Lottmann S., Thomassen R.;
 RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
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CC EMBL; X51970; CAA36232.1;
 DR PIR; S10381; NKVLKS.
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 193 200
 FT REPEAT 201 208
 FT REPEAT 214 214

SQ SEQUENCE 214 AA; 24722 MW; 2D668333EC5AFB8C CRC64;

Query Match 93.8%; Score 165; DB 1; Length 214;
 Best Local Similarity 94.1%; Pred. No. 1.3e-11;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
 |||||
 DB 181 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 214

RESULT 10

CORA_HPBVL STANDARD; PRT; 183 AA.
 ID AC P12901;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE CORE ANTIGEN.
 GN C.

OS Hepatitis B virus (strain lsh / chimpanzee isolate).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10414;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88258473; PubMed=2838576;
 RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
 RA Harrison T.J.;
 RT "The complete nucleotide sequence of the genome of a hepatitis B
 RT virus isolated from a naturally infected chimpanzee.";
 RL J. Gen. Virol. 69:1383-1389(1988).

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CC EMBL; D00220; BAA00157.1;
 DR PIR; A28885; NKVLCF.
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.

KW Core protein; Repeat.
 FT REPEAT 162 169
 FT REPEAT 170 177

SQ SEQUENCE 183 AA; 20999 MW; 923DCB94A33FC0E8 CRC64;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34
 |||||
 DB 150 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

Query Match 90.3%; Score 159; DB 1; Length 183;
 Best Local Similarity 91.2%; Pred. No. 4.8e-11;
 Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 11
COR_AHPBV2
ID COR_AHPBV2 STANDARD; PRT; 212 AA.
AC Q05495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RI Identification of a new hepatitis B virus (HBV) genotype from Brazil
RI that expresses HBV surface antigen subtype adw4.;
RL J. Gen. Virol. 74:1627-1632(1993).
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CC -----
DR EMBL; X59798; GAA49452.1;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Repeat.
KW Core protein; Repeat.
FT DOMAIN 178 204 ARG-RICH.
FT DOMAIN 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.
FT REPEAT 184 188 1.
FT REPEAT 191 195 2.
FT REPEAT 199 203 3.
SQ SEQUENCE 212 AA; 24234 MW; F832610DB7C36FD2 CRC64;

Query Match 90.3%; Score 159; DB 1; Length 212;
Best Local Similarity 91.2%; Pred. No. 5.5e-11;
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRSQC 34
Db 179 RRGSRPRRTSPRRRSKSPRRRSQSRSQC 212

RESULT 12
COR_AHPBV2
ID COR_AHPBV2 STANDARD; PRT; 185 AA.
AC P03148;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Hepatitis B virus (subtype adw2).
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RX Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (in) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
DR PIR; A94409; NKVLA3.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179

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SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 89.8%; Score 158; DB 1; Length 185;
Best Local Similarity 91.2%; Pred. No. 6.2e-11;
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRSQC 34
Db 152 RRGSRPRRTSPRRRSKSPRRRSQSRSQC 185

RESULT 13
COR_AHPBV2
ID COR_AHPBV2 STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Ground squirrel hepatitis virus (GSV).
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10406;
RN [1]
RP SEQUENCE FROM N.A.
RX METLINE=84267998; PubMed=6086950;
RA Seeger C., Ganem D., Varmus H.E.;
RI "Nucleotide sequence of an infectious molecularly cloned genome of
RI ground squirrel hepatitis virus.";
RL J. Virol. 51:367-375(1984).
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CC -----
DR EMBL; X02715; AAA46755.1;
DR PIR; A03715; NKVLS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; DF489467355ECL1A CRC64;

Query Match 80.4%; Score 141.5; DB 1; Length 217;
Best Local Similarity 76.9%; Pred. No. 4.3e-09;
Matches 30; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRSQC 34
Db 179 RRGSRPRRTSPRRRSKSPRRRSQSRSQC 217

RESULT 14
COR_AHPBV2
ID COR_AHPBV2 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Woodchuck hepatitis virus 1 (WHV 1).
OS Woodchuck hepatitis virus 7 (WHV 7).
OS Woodchuck hepatitis virus 59 (WHV 59), and
OS Woodchuck hepatitis virus 8 (infectious clone) (WHV 8).
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

```

```
OX NCBI_TaxID=10430, 10432, 10431, 10434;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Woodchuck hepatitis virus 1;
RX MEDLINE=8221986; PubMed=7066958;
RA Galibert F., Chen T.N., Mandart B.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RL comparison with the hepatitis B virus sequence.";
RJ J. Virol. 41:51-65(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Woodchuck hepatitis virus 7, and Woodchuck hepatitis virus 59;
RX MEDLINE=88101359; PubMed=3336938;
RA Cohen J.I., Miller R.H., Rosenblum B., Denniston K., Gerin J.L.,
RJ Purcell R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RL shows conservation of the genome.";
RJ Virology 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Woodchuck hepatitis virus 8 (Infectious clone);
RX MEDLINE=89184524; PubMed=2328306;
RA Grimes R., Cote P.J., Hornbuckle W.E., Tennant B.C., Gerin J.L.,
RJ Purcell R.H., Miller R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RL hepatitis virus that is infectious in the natural host.";
RJ Proc. Natl. Acad. Sci. U.S.A. 86:1846-1849(1989).
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CC -----
DR EMBL: J02442; AAA46761.1;
DR EMBL: M18752; AAA46769.1;
DR EMBL: M19183; AAA46765.1;
DR EMBL: J04514; AAA46772.1;
DR FIR: A03713; NKVLC.
DR FIR: C32397; NKVLC.
DR FIR: C32397; NKVLC.
DR FIR: C32397; NKVLC.
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; 1F4454D0A7B7CE42 CRC64;

Query Match 79.3%; Score 139.5; DB 1; Length 188;
Best Local Similarity 74.4%; Pred. No. 6.2e-09;
Matches 29; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

OY 1 RRRG-----RRSPRRTPSPRRRSKSPRRRSQSRESQC 34
Db 150 RRRGARRSKSPRRTPSPRRRSKSPRRRSQSRESQC 188

RESULT 15
CORA_WHV8
ID CORA_WHV8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Woodchuck hepatitis virus 8 (WHV 8).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10433;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86062931; PubMed=3855246;
RA Kodama K., Ogasawara N., Yoshikawa H., Murakami S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RJ evolutionary relationship between hepadnaviruses.";
RJ J. Virol. 56:1978-1986(1985).
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CC -----
DR EMBL: M1082; AAA19185.1;
DR FIR: A03714; NKVLC2.
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 166 173
FT REPEAT 174 181
SQ SEQUENCE 187 AA; 21579 MW; D4BC446FF7163165 CRC64;

Query Match 76.7%; Score 135; DB 1; Length 187;
Best Local Similarity 78.8%; Pred. No. 1.9e-08;
Matches 26; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 RRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
Db 155 RASRSPRRTPSPRRRSKSPRRRSQSRESQC 187

Search completed: April 18, 2002, 09:28:49
Job time: 117 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 13.49 Seconds
(without alignments)
191.989 Million cell updates/sec

Title: US-08-841-657A-2

Perfect score: 176

Sequence: 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	100.0	183	2 S53152	core antigen - hep
2	172	97.7	183	1 NKVLA2	core antigen - hep
3	172	97.7	183	2 S53232	core antigen - hep
4	172	97.7	183	2 S53247	core antigen - hep
5	172	97.7	183	2 S53267	core antigen - hep
6	172	97.7	183	2 S53149	core antigen - hep
7	172	97.7	183	2 S53194	core antigen - hep
8	172	97.7	183	2 S53181	core antigen - hep
9	172	97.7	183	2 S22318	core antigen - hep
10	172	97.7	212	1 NKVLAH	e antigen precursor
11	172	97.7	212	1 NKVLBH	e antigen precursor
12	172	97.7	212	1 NKVLA4	e antigen precursor
13	172	97.7	212	1 NKVLJ1	e antigen precursor
14	172	97.7	212	1 NKVLJ2	e antigen precursor
15	172	97.7	212	2 S53211	e antigen precursor
16	172	97.7	212	2 S53216	e antigen precursor
17	172	97.7	212	2 S53223	e antigen precursor
18	172	97.7	212	2 S53225	e antigen precursor
19	172	97.7	212	2 S53229	e antigen precursor
20	172	97.7	212	2 S53236	e antigen precursor
21	172	97.7	212	2 S53238	e antigen precursor
22	172	97.7	212	2 S53240	e antigen precursor
23	172	97.7	212	2 S53242	e antigen precursor
24	172	97.7	212	2 S53251	e antigen precursor
25	172	97.7	212	2 S53253	e antigen precursor
26	172	97.7	212	2 S53255	e antigen precursor
27	172	97.7	212	2 S53257	e antigen precursor
28	172	97.7	212	2 S53272	e antigen precursor
29	172	97.7	212	2 S53274	e antigen precursor

30	172	97.7	212	2 S53279	e antigen precursor
31	172	97.7	212	2 S20746	e antigen precursor
32	172	97.7	212	2 S32204	e antigen precursor
33	172	97.7	212	2 S20750	e antigen precursor
34	172	97.7	212	2 S53159	e antigen precursor
35	172	97.7	212	2 S53163	e antigen precursor
36	172	97.7	212	2 S53168	e antigen precursor
37	172	97.7	212	2 S53202	e antigen precursor
38	172	97.7	212	2 S53227	e antigen precursor
39	172	97.7	359	2 S04570	gene X/C fusion pr
40	170	96.6	195	1 NKVLH3	core antigen - hep
41	169	96.0	183	2 S53214	core antigen - hep
42	169	96.0	183	2 S53270	core antigen - hep
43	169	96.0	183	2 S53155	core antigen - hep
44	169	96.0	183	2 S53166	core antigen - hep
45	169	96.0	183	2 S53169	core antigen - hep

ALIGNMENTS

RESULT 1
S53152
core antigen - hepatitis B virus (isolate patient Tufariello'89)
N:Alternate names: HBC antigen
N:Contains: core antigen
C:Species: Hepatitis B virus, HBV
A:Variety: Isolate patient Tufariello'89
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53152
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53152
A:Molecule type: DNA
A:Residues: 1-183 <LAI>
A:Cross-references: EMBL:X85269; NID:g736033; PIDN:CAA59556.1; PID:g736036
A:Experimental source: Isolate patient Tufariello'89
A:Note: due to a stop codon between the alternative initiators the e antigen precursor
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: core protein

Query Match 100.0%; Score 176; DB 2; Length 183;
Best local Similarity 100.0%; Pred. NO. 4e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34
|||||
DB 150 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 183

RESULT 2
NKVLA2
core antigen - hepatitis B virus (subtype adyw)
C:Species: hepatitis B virus, HBV
A:Variety: subtype adyw
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
R:Pasek, M.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; Mackay, P.; Leadbetter, G.
Nature 382, 575-579, 1979
A:Title: Hepatitis B virus genes and their expression in E. coli.
A:Reference number: A93217; MUID:81012115
A:Accession: B93217
A:Molecule type: DNA
A:Residues: 1-183 <PAS>
A:Cross-references: GB:J02202; NID:g329637; PIDN:AAA5486.1; PID:g329638
A:Experimental source: subtype adyw
A:Note: due to a stop codon between the alternative initiators the e antigen precursor
C:Genetics:
A:Gene: C

C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein
F;1-183/Product: core antigen #status predicted

Query Match 97.7%; Score 172; DB 1; Length 183;
Best Local Similarity 97.1%; Pred. No. 1e-10;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 RRRGSPRRRTSPRRRRKSPRRRSQSRESQC 34  
       |||||  
Db     150 RRRGSPRRRTSPRRRRSQSPRRRSQSRESQC 183
```

RESULT 3
S53232
core antigen - hepatitis B virus (isolate patient Dettori-2'87)
N:Alternate names: HBC antigen
N:Contains: core antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Dettori-2'87
C:Date: 08-Jul-1995 sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53232
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
Submitted to the EMBL Data Library, March 1995
A:Reference number: S53112

A:Note: due to a stop codon between the alternative initiators the e antigen precursor is not translated.

```
QY 1 RRGCSPPRRTPSPRRRRSKSPRRRRSQSRSSQC 34
    |||||
Db 150 RRGCSPPRRTPSPRRRRSQSRSSQC 183
```

RESULT 4
SS3247
core antigen - hepatitis B virus (isolate patient Flore-2'91)
N:Alternate names: Hbc antigen
N:Contains: core antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Flore-2'91
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: SS3247
Submitted to the EMBL Data Library, March 1995
A:Reference number: S53112

Query Match 97.7%; Score 172; DB 2; Length 183;
Best Local Similarity 97.1%; Pred. No. 1e-10;

Matches	33: Conservative	1: Mismatches	0: Indels
1	RRGRSPRRTSPRRRSKSPRRRSQ	34	
150	RRGRSPRRTSPRRRSKSPRRRSQ	183	
db	RRGRSPRRTSPRRRSKSPRRRSQ	183	

RESULT 5
S53267
core antigen - hepatitis B virus (isolate patient Lucianoc'92)
N/Alternate names: Hbc antigen
N/Contains: core antigen
C.Species: hepatitis B virus, HBV
A.Variety: isolate patient Lucianoc'92
C.Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C.Accession: S53267
R.Lai, M.B.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
Submitted to the EMBL Data Library, March 1995
A.Reference number: S53112
A.Accession: S53267

Query Match 97.7%; Score 172; DB 2; Length 183;
Best Local Similarity 97.1%; Pred. No. 1e-10;
Matches 33; Conservative 1; Mismatches 0; Indels

```

1  RRRGRSPRRRTSPRRRRSKSPRRRRSQSRRESQC 34
   |||||
150 RRRGRSPRRRTSPRRRRSKSPRRRRSQSRRESQC 183

```

RESULT 6
S53149
core antigen - hepatitis B virus (isolate patient Sini'90)
Alternate names: HBC antigen
N:Contains: core antigen
C:Species: hepatitis B virus. HBV
A:Variety: isolate patient Sini'90
Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
Accession: S53149
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
Submitted to the EMBL Data Library, March 1995
A:Reference number: S53112

Query Match	97.7%	Score 172;	DB 2;	Length 183;
Best Local Similarity	97.1%	Pred. No. 1e-10;		

1 RRRGRSPRRRTSPRRRRSKSPRRRRSQSRSSQC 34
 |||||
 150 RRRGRSPRRRTSPRRRRSQSPRRRRSQSRSSQC 183
 |||||

RESULT 7
 S53194
 core antigen - hepatitis B virus (isolate patient Italoc/92)
 N:Alternate names: HBC antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Italoc/92
 C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Accession: S53194
 A:Reference number: S53112
 A:Molecule type: DNA
 A:Residues: 1-183 <LA1>
 A:Cross-references: EMBL:X85257; NID:g736091; PIDN:CAA59522.1; PID:g736094
 A:Experimental source: isolate patient Italoc/92
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;
 Best Local Similarity 97.1%; Pred. No. 1e-10;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSKSPRRRSQRESQC 34
 |||||
 Db 150 RRGSRPRRTTSPRRRSKSPRRRSQRESQC 183

RESULT 8
 S53181
 core antigen - hepatitis B virus
 N:Alternate names: HBC antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Molecule type: DNA
 A:Residues: 1-183 <LA1>
 A:Cross-references: EMBL:X85279; NID:g736073; PIDN:CAA59593.1; PID:g736076
 A:Experimental source: isolate patient Bitti/89
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;
 Best Local Similarity 97.1%; Pred. No. 1e-10;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSKSPRRRSQRESQC 34
 |||||
 Db 150 RRGSRPRRTTSPRRRSKSPRRRSQRESQC 183

RESULT 9
 S22318
 core antigen - hepatitis B virus (subtyp ayw, isolate Sardinia)

N:Alternate names: HBC antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: subtyp ayw, isolate Sardinia
 C>Date: 19-Feb-1994 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
 R:Lai, M.E.; Mellis, A.; Mazzoleni, A.P.; Farci, P.; Balestrieri, A.
 Nucleic Acids Res. 19, 5076, 1991
 A:Title: Sequence analysis of hepatitis B virus genome of a new mutant of ayw subtype
 A:Reference number: S22317; MUID:192020153
 A:Accession: S22318
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-183 <LA1>
 A:Cross-references: EMBL:X59795; NID:g313780; PIDN:CAA42464.1; PID:g313782
 A:Experimental source: subtyp ayw, isolate Sardinia
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;
 Best Local Similarity 97.1%; Pred. No. 1e-10;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSKSPRRRSQRESQC 34
 |||||
 Db 150 RRGSRPRRTTSPRRRSKSPRRRSQRESQC 183

RESULT 10
 NKVLAH
 core antigen - hepatitis B virus (subtyp ayw4, isolate hb321 a
 N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
 N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: subtyp ayw4, isolate hb321; isolate patient Ferracuti/83; isolate patient
 Cheri/83
 C>Date: 18-Dec-1991 #sequence_revision 08-Nov-1996 #text_change 16-Jul-1999
 C:Accession: S47405; S53191; S53209; S53234; S53264; S53249; S53262; S53277; A03711
 R:Plucieniczak, A.
 submitted to the EMBL Data Library, August 1994
 A:Description: Molecular cloning and sequencing of two complete genomes of polish iso
 A:Reference number: S47404
 A:Molecule type: DNA
 A:Residues: 1-212 <PLD>
 A:Cross-references: EMBL:X527435; PIDN:CAA84786.1; PID:g527437
 A:Experimental source: subtyp ayw4, isolate hb321
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Molecule type: DNA
 A:Residues: 1-212 <LA1>
 A:Cross-references: EMBL:X85283; NID:g736088; PIDN:CAA59593.1; PID:g736090
 A:Experimental source: isolate patient Ferracuti/83
 A:Accession: S53209
 A:Molecule type: DNA
 A:Residues: 1-212 <LA2>
 A:Cross-references: EMBL:X85290; NID:g736114; PIDN:CAA59609.1; PID:g736116
 A:Experimental source: isolate patient Castag/83
 A:Accession: S53234
 A:Molecule type: DNA
 A:Residues: 1-212 <LA3>
 A:Cross-references: EMBL:X85300; NID:g736150; PIDN:CAA59631.1; PID:g736152
 A:Experimental source: isolate patient Sanna/84
 A:Accession: S53264
 A:Molecule type: DNA
 A:Residues: 1-212 <LA4>
 A:Cross-references: EMBL:X85313; NID:g736194; PIDN:CAA59659.1; PID:g736196

A:Experimental source: isolate patient Licheri-1'85

A:Accession: S53249

A:Molecule type: DNA

A:Residues: 1-212 <LA5>

A:Cross-references: EMBL:X85306; NID:g736172; PIDN:CAA59644.1; PID:g736174

A:Experimental source: isolate patient Flore-1'86

A:Accession: S53262

A:Molecule type: DNA

A:Residues: 1-212 <LA6>

A:Cross-references: EMBL:X85312; NID:g736191; PIDN:CAA59657.1; PID:g736193

A:Experimental source: isolate patient Licheri'83

A:Accession: S53277

A:Molecule type: DNA

A:Residues: 30-212 <LA7>

A:Cross-references: EMBL:X85317; NID:g736211; PIDN:CAA59669.1; PID:g736214

A:Experimental source: patient Giordo-2'86

A:Note: due to a stop codon between the alternative initiators the e antigen precursor d

R:Galibert, F.; Wandert, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.

Nature 281, 646-650, 1979

A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.

A:Reference number: A93711

A:Accession: A03711

A:Molecule type: DNA

A:Residues: 1-212 <GAL>

A:Cross-references: GB:J02203; NID:g329640; PIDN:AAA45489.1; PID:g329642

A:Experimental source: subtype ayw

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match

Best Local Similarity 97.7%; Score 172; DB 1; Length 212;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGGRSPRRTPSPRRRSQSRESQC 34

|||||

DB 179 RRGGRSPRRTPSPRRRSQSRESQC 212

RESULT 11

NKVLBH

e antigen precursor / core antigen - hepatitis B virus (subtype ayw, strain PHB320)

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

C:Species: hepatitis B virus, HBV

A:Variety: subtype ayw, strain PHB320

A:Note: host *Homo sapiens* (man)

C:Date: 17-Mar-1987 #sequence,revision 08-Nov-1996 #text_change 28-Jul-2000

C:Accession: A03712

R:Richko, V.; Pushko, P.; Drellina, D.; Pumpen, P.; Gren, E.

FEBS Lett. 185, 208-212, 1985

A:Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.

A:Reference number: A05237; MUID:85204397

A:Accession: A03712

A:Molecule type: DNA

A:Residues: 1-212 <BIC>

A:Cross-references: GB:X02496; NID:g62280; PIDN:CAB41698.1; PID:g4704318

A:Experimental source: subtype ayw, strain PHB320

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match

Best Local Similarity 97.7%; Score 172; DB 1; Length 212;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGGRSPRRTPSPRRRSQSRESQC 34

|||||

DB 179 RRGGRSPRRTPSPRRRSQSRESQC 212

RESULT 12

NKVLBH

e antigen precursor / core antigen - hepatitis B virus (subtype adr and others)

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

C:Species: hepatitis B virus, HBV

A:Variety: subtypes adr; adw; 09009HCC

C:Date: 30-Jun-1992 #sequence,revision 08-Nov-1996 #text_change 28-Jul-2000

C:Accession: A93480; C28925; B93460; S35530; T13467; A03711

R:Fujiyama, A.; Miyanochara, A.; Nozaki, C.; Yoneyama, T.; Ontomo, N.; Matsubara, K.

Nucleic Acids Res. 11, 4601-4610, 1983

A:Title: Cloning and structural analyses of hepatitis B virus DNAs, subtype adr.

A:Reference number: A93480; MUID:83246570

A:Accession: A93480

A:Molecule type: DNA

A:Residues: 1-212 <FUJ>

A:Cross-references: GB:X01587; NID:g59404; PIDN:CAA25745.1; PID:g59407

A:Experimental source: subtype adr4

R:Okamoto, H.; Tsuda, F.; Sakagawa, H.; Sastrosoewignjo, R.I.; Inai, M.; Miyakawa, Y.

J. Gen. Virol. 69, 2575-2583, 1988

A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of s

A:Reference number: J50253; MUID:89010694

A:Accession: C28925

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <OKA>

A:Cross-references: EMBL:D00331; NID:g221499

A:Experimental source: subtype adr, strain Indonesia/PIDW420

R:Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Sugino, Y.; Nishioka, K.

Nucleic Acids Res. 11, 1747-1757, 1983

A:Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subty

A:Reference number: A93460; MUID:83168919

A:Accession: B93460

A:Molecule type: DNA

A:Residues: 30-212 <ONO>

A:Cross-references: GB:V00867

A:Experimental source: subtype adr

A:Note: due to a missing start codon for pre-C the e antigen precursor cannot be prod

R:Mukaida, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hikiji, K.

Nucleic Acids Res. 20, 6105, 1992

A:Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) a

A:Reference number: S35527; MUID:93096607

A:Accession: S35530

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <MUK>

A:Cross-references: EMBL:D12980; NID:g221500; PIDN:BAA02357.1; PID:g221504

A:Experimental source: subtype adr

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R:Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishiro, S.

Arch. Virol. 143, 2313-2326, 1998

A:Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carc

A:Reference number: 217684; MUID:99129050

A:Accession: T13467

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-212 <TAK>

A:Cross-references: EMBL:AB014368; NID:g3551304; PIDN:BAA32862.1; PID:g3551306

A:Experimental source: Japanese patient with hepatocellular carcinoma isolate 09D09HC

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 1; Length 212;
Best Local Similarity 97.1%; Pred. No. 1.1e-10;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
|||||
Db 179 RRRGSPRRTPSPRRRSQSPPRRRSQSRESQC 212
|||||

RESULT 13
NKVLJ1
e antigen precursor / core antigen - hepatitis B virus (subtype adv, strain Japan/pJDM23)
N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype adv, strain Japan/pJDM233
C:Date: 31-Mar-1990 #sequence_revision 08-Nov-1996 #text_change 14-Nov-1997
C:Accession: A28925
R:Okamoto, H.; Tada, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; M
J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur
A:Reference number: JS0253; MUID:89010694
A:Accession: A28925
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-212 <OKA>
A:Cross-references: EMBL:D00329; NID:g221498
A:Experimental source: subtype adv, strain Japan/pJDM233
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 1; Length 212;
Best Local Similarity 97.1%; Pred. No. 1.1e-10;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
|||||
Db 179 RRRGSPRRTPSPRRRSQSPPRRRSQSRESQC 212
|||||

RESULT 14
NKVLJ2
e antigen precursor / core antigen - hepatitis B virus (subtype adv, strain Okinawa/pODM
N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype adv, strain Okinawa/pODM282
C:Date: 31-Mar-1990 #sequence_revision 08-Nov-1996 #text_change 14-Nov-1997
C:Accession: B28925
R:Okamoto, H.; Tada, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; M
J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur
A:Reference number: JS0253; MUID:89010694
A:Accession: B28925
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-212 <OKA>
A:Cross-references: EMBL:D00330; NID:g221498
A:Experimental source: subtype adv, strain Okinawa/pODM282
C:Genetics:

A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 1; Length 212;
Best Local Similarity 97.1%; Pred. No. 1.1e-10;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
|||||
Db 179 RRRGSPRRTPSPRRRSQSPPRRRSQSRESQC 212
|||||

RESULT 15
SS3211
e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag-1'85 a
N:Alternate names: HBe antigen; HBe antigen precursor / HBe antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Castag-1'85; isolate patient Ferracuti-1'89
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53197
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53211
A:Molecule type: DNA
A:Residues: 1-212 <LAW>
A:Cross-references: EMBL:X85291; NID:g736117; PIDN:CAA59611.1; PID:g736119
A:Experimental source: isolate patient Castag-1'85
A:Accession: S53197
A:Molecule type: DNA
A:Residues: 30-212 <LAW>
A:Cross-references: EMBL:X85284; NID:g736095; PIDN:CAA59596.1; PID:g736098
A:Experimental source: isolate patient Ferracuti-1'89
A:Note: due to a stop codon between the alternative initiators the e antigen precurs
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 2; Length 212;
Best Local Similarity 97.1%; Pred. No. 1.1e-10;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34
|||||
Db 179 RRRGSPRRTPSPRRRSQSPPRRRSQSRESQC 212
|||||

Search completed: April 18, 2002, 09:27:44
Job time: 52 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 22.03 Seconds
(without alignments)
225.749 Million cell updates/sec

Title: US-08-841-657A-2

Perfect score: 176

Sequence: 1 RRRGSPRRPTSPRRRRSKSPRRRSQSRSSQC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.priant.*
- 12: sp.virus.*
- 13: sp.vertbrate.*
- 14: sp.unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	96	12	Q9YL95 hepatitis b
2	176	100.0	183	12	Q9YL92 hepatitis b
3	176	100.0	183	12	Q9YL93 hepatitis b
4	172	97.7	157	12	Q9YL99 hepatitis b
5	172	97.7	163	12	Q9YL98 hepatitis b
6	172	97.7	183	12	Q9YL97 hepatitis b
7	172	97.7	183	12	Q9YL96 hepatitis b
8	172	97.7	183	12	Q9YL94 hepatitis b
9	172	97.7	183	12	Q9YL93 hepatitis b
10	172	97.7	183	12	Q9YL92 hepatitis b
11	172	97.7	183	12	Q9YL91 hepatitis b
12	172	97.7	183	12	Q9YL90 hepatitis b
13	172	97.7	183	12	Q9YL89 hepatitis b
14	172	97.7	183	12	Q9YL88 hepatitis b
15	172	97.7	183	12	Q9YL87 hepatitis b
16	172	97.7	183	12	Q9YL86 hepatitis b
17	172	97.7	183	12	Q9YL85 hepatitis b
18	172	97.7	183	12	Q9YL84 hepatitis b
19	172	97.7	183	12	Q9YL83 hepatitis b

20	172	97.7	183	12	Q9YL95
21	172	97.7	183	12	Q9YL92
22	172	97.7	183	12	Q9YL93
23	172	97.7	183	12	Q9YL99
24	172	97.7	183	12	Q9YL98
25	172	97.7	183	12	Q9YL97
26	172	97.7	183	12	Q9YL96
27	172	97.7	183	12	Q9YL94
28	172	97.7	183	12	Q9YL93
29	172	97.7	183	12	Q9YL92
30	172	97.7	183	12	Q9YL91
31	172	97.7	183	12	Q9YL90
32	172	97.7	183	12	Q9YL89
33	172	97.7	183	12	Q9YL88
34	172	97.7	183	12	Q9YL87
35	172	97.7	183	12	Q9YL86
36	172	97.7	183	12	Q9YL85
37	172	97.7	183	12	Q9YL84
38	172	97.7	183	12	Q9YL83
39	172	97.7	183	12	Q9YL82
40	172	97.7	183	12	Q9YL81
41	172	97.7	183	12	Q9YL80
42	172	97.7	183	12	Q9YL79
43	172	97.7	183	12	Q9YL78
44	172	97.7	183	12	Q9YL77
45	172	97.7	183	12	Q9YL76

ALIGNMENTS

RESULT 1
Q9YL95
ID Q9YL95 PRELIMINARY; PRT; 96 AA.
AC Q9YL95
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CORE ANTIGEN (FRAGMENT)
OS C.
GN Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GENOTYPE D;
RA Manzin A.;
RT *An outbreak of fulminant hepatitis B in a haematologic unit (Pesaro, Italy), part 2.*
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010007; CAA08962.1; -
DR EMBL; AJ009994; CAA08936.1; -
DR EMBL; AJ009995; CAA08938.1; -
DR EMBL; AJ009996; CAA08940.1; -
DR EMBL; AJ009997; CAA08942.1; -
DR EMBL; AJ009998; CAA08944.1; -
DR EMBL; AJ009999; CAA08946.1; -
DR EMBL; AJ010000; CAA08948.1; -
DR EMBL; AJ010001; CAA08950.1; -
DR EMBL; AJ010002; CAA08952.1; -
DR EMBL; AJ010003; CAA08954.1; -
DR EMBL; AJ010004; CAA08956.1; -
DR EMBL; AJ010005; CAA08958.1; -
DR EMBL; AJ010006; CAA08960.1; -
DR Interpro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
SQ SEQUENCE 96 AA; 11443 MW; FEA862E745196B9E CRC64;

Query Match 100.0%; Score 176; DB 12; Length 96;
Best Local Similarity 100.0%; Pred. No. 8.2e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34
 DB 63 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 96

RESULT 2
 Q67973
 ID Q67973 PRELIMINARY; PRT; 183 AA.

AC Q67973;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE X, PREC AND C GENES (TUFARIELLO).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT TUFARIELLO/89;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85269; CAA59556.1;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21072 MW; 4E06CF2F539199A3 CRC64;

Query Match 100.0%; Score 176; DB 12; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34
 DB 150 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 3
 Q81102
 ID Q81102 PRELIMINARY; PRT; 183 AA.

AC Q81102;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE CORE ANTIGEN.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-83168919; PubMed-6300776;
 RA Ono T., Chida H., Sasada K., Igarashi K., Sugino Y., Mishioka K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 DNA; subtype adr and adw.";
 RL Nucleic Acids Res. 11:1747-1757(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-85077616; PubMed-6510717;
 RA Kobayashi M., Koike K.;
 RT "Complete nucleotide sequence of hepatitis B virus DNA of subtype adr
 and its conserved gene organization.";
 RL Gene 30:227-232(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-90356395; PubMed-2388835;
 RA Takemura F., Ishii T., Fujii N., Uchida T.;
 RT "Complete nucleotide sequence of hepatitis B virus.";
 RL Nucleic Acids Res. 18:4587-4587(1990).
 DR EMBL; D00630; BAA00523.1;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21102 MW; B32B2BF3AF7ED4E8 CRC64;

Query Match 100.0%; Score 176; DB 12; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34
 DB 150 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4
 Q991J9
 ID Q991J9 PRELIMINARY; PRT; 157 AA.

AC Q991J9;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE PRECORE/CORE PROTEIN.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dong J., Cheng J., Wang Q., Wang G., Shi S., Zhang J., Xia X., Si C.;
 RT "HBV quasisppecies; prec/C region as example.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF33747; AAK30091.1;
 SQ SEQUENCE 157 AA; 18109 MW; DE48B1F77AA52F8A CRC64;

Query Match 97.7%; Score 172; DB 12; Length 157;
 Best Local Similarity 97.1%; Pred. No. 3.7e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34
 DB 124 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 157

RESULT 5
 Q91HC8
 ID Q91HC8 PRELIMINARY; PRT; 163 AA.

AC Q91HC8;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE PRE-CORE/CORE PROTEIN.
 OS Hepatitis B virus (subtype adw2).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADW2;
 RA Cheng T., Chen M., Zhang J., Xia N.S.;
 RT "HBV genome sequence from patient's serum of Xiamen, Fujian, China.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF233236; AAF82722.1;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 2.
 SQ SEQUENCE 163 AA; 18565 MW; 5D2E668C43076FFE CRC64;

Query Match 97.7%; Score 172; DB 12; Length 163;
 Best Local Similarity 97.1%; Pred. No. 3.8e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34
 DB 130 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 163

RESULT 6
 Q89437

ID Q89437 PRELIMINARY; PRT; 183 AA.
 AC Q89437;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE X, PREC AND C GENES (CASTAA 2).
 GN CORE.
 OS Hepatitis B virus (subtype ayw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10418;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-PATIENT CASTAA-2'87;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AYW;
 RA Karayiannis P.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85289; CAA59607.1; -;
 DR EMBL; X80925; CAA56888.1; -;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1
 SQ SEQUENCE 183 AA; 21102 MW; 2B8902063F253228 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 34
 |||||
 Db 150 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 7
 Q67970
 ID Q67970 PRELIMINARY; PRT; 183 AA.
 AC Q67970;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE X, PREC AND C GENES (SINI).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-PATIENT SINI'90;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85268; CAA59553.1; -;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1
 SQ SEQUENCE 183 AA; 21108 MW; A3C21BD403676FF5 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 34
 |||||
 Db 150 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 8
 Q67997
 ID Q67997 PRELIMINARY; PRT; 183 AA.
 AC Q67997;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE X, PREC AND C GENES (BITTI).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-PATIENT BITTI'89;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85279; CAA59583.1; -;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1
 SQ SEQUENCE 183 AA; 21158 MW; F74F9B9B2FF90D7C CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 34
 |||||
 Db 150 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 9
 Q68006
 ID Q68006 PRELIMINARY; PRT; 183 AA.
 AC Q68006;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE X, PREC AND C GENES (ITALOC).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-PATIENT ITALOC'92;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85257; CAA59522.1; -;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1
 SQ SEQUENCE 183 AA; 20996 MW; E391589B6AD747AF CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 34
 |||||
 Db 150 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 183

RESULT 10
 Q68008
 ID Q68008 PRELIMINARY; PRT; 183 AA.
 AC Q68008;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE X, PREC AND C GENES (FERRACUTI 1).
 GN CORE.

OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT FERRACUTI-1'89;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85284; CAA59596.1;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21102 MW; 50D8D9763F75E958 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 34
 |||||
 DB 150 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 183

RESULT 11
 Q68037 ID Q68037 PRELIMINARY; PRT; 183 AA.
 AC Q68037;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE X, PREC AND C GENES (DETORI 2).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT DETORI-2'87;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85299; CAA59629.1;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21161 MW; CD85663FE5F8B833 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 34
 |||||
 DB 150 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 183

RESULT 12
 Q68048 ID Q68048 PRELIMINARY; PRT; 183 AA.
 AC Q68048;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE X, PREC AND C GENES (FLORE 2).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT FLORE-2'91;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85305; CAA59642.1;
 SQ SEQUENCE 183 AA; 21102 MW; 885DB61DADA412AA CRC64;

DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21132 MW; E66F00FABBE4258 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 34
 |||||
 DB 150 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 183

RESULT 13
 Q68064 ID Q68064 PRELIMINARY; PRT; 183 AA.
 AC Q68064;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE X, PREC AND C GENES (LUCIANOC).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT LUCIANOC'92;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85260; CAA59530.1;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21022 MW; E679001806718CCE CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 34
 |||||
 DB 150 RRGSRPRRTTSPRRRSQSPRRRSQSRSSQC 183

RESULT 14
 Q68083 ID Q68083 PRELIMINARY; PRT; 183 AA.
 AC Q68083;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE HEPATITIS B VIRUS X, PREC AND C GENES (AMOROSO).
 GN CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT AMOROSO'89;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85263; CAA59538.1;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21208 MW; 885DB61DADA412AA CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGGRPRRTSPRRRSKSPRRRSQSRESQC 34
 DB 150 RRGGRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 15

Q69597 PRELIMINARY; PRT; 183 AA.
 AC Q69597;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE CORE PROTEIN.
 GN C.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GENOTYPE C;
 RX MEDLINE=94120723; PubMed=8291231;
 RA Nordier H., Courouce A.M., Magnius L.O.;
 RT "Complete genomes, phylogenetic relatedness, and structural proteins
 of six strains of the hepatitis B virus, four of which represent two
 new genotypes.";
 RL Virology 198;489-503(1994).
 DR EMBL; X75665; CAA53361.1;
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1
 SQ SEQUENCE 183 AA; 21081 MW; ED2DB34B0A6B466D CRC64;

Query Match 97.78; Score 172; DB 12; Length 183;
 Best Local Similarity 97.18; Pred. No. 4.2e-14;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGGRPRRTSPRRRSKSPRRRSQSRESQC 34
 Db 150 RRGGRPRRTSPRRRSKSPRRRSQSRESQC 183

Search completed: April 18, 2002, 09:28:32
 Job time: 100 sec